

123-03_US_second_replacement_sequence.txt
SEQUENCE LISTING

<110> Hexima Limited
Poon, Simon
Heath, Robyn L.
Clarke, Adrienne E.

<120> Arabinogalactan Protein Compositions and Methods for Fostering Somatic Embryonic Competence

<130> 12639240/AJH

<140> 10/594,418

<141> 2005-03-31

<150> 60/558,609

<151> 2004-03-01

<160> 27

<170> PatentIn version 3.4

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Ser Thr Ala Ser Leu Gly Val Thr Leu Ser Val
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Ile Gln Val Xaa Asp Glu Val Xaa Glu
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tcttctgaat cagattctct caacaaatgg gctgaaaaag ctcgtttcca aatcggcgac 180
tctctcgtgt gaaaaatatga tgggtgtaaa gactcggtgc tccaaagttagtga 240
tataacaagtt gcaatacgtc gaacccgatt gccgagtaca aagatggaa caccaaggtg 300
aagcttgaaa agtcaggacc atatttcttc atgagtggag caaaggggcca ctgcgagcaa 360
ggccagaaga tgattgtggt tgtgatgtct caaaagcata ggtacattgg aatctctcca 420
gcacccctcgc cggttgattt tgaaggtccg gccgttgctc caacaagcgg agttgcaggg 480
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<212> PRT
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1 5 10 15

Phe Ile Phe Leu Ser Phe Ala Gln Gly Lys Glu Ile Met Val Gly Gly
20 25 30

Lys Thr Gly Ala Trp Lys Ile Pro Ser Ser Glu Ser Asp Ser Leu Asn
35 40 45

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Lys Trp Ala Glu Lys Ala Arg Phe Gln Ile Gly Asp Ser Leu Val Trp
50 55 60

Lys Tyr Asp Gly Gly Lys Asp Ser Val Leu Gln Val Ser Lys Glu Asp
65 70 75 80

Tyr Thr Ser Cys Asn Thr Ser Asn Pro Ile Ala Glu Tyr Lys Asp Gly
85 90 95

Asn Thr Lys Val Lys Leu Glu Lys Ser Gly Pro Tyr Phe Phe Met Ser
100 105 110

Gly Ala Lys Gly His Cys Glu Gln Gly Gln Lys Met Ile Val Val Val
115 120 125

Met Ser Gln Lys His Arg Tyr Ile Gly Ile Ser Pro Ala Pro Ser Pro
130 135 140

Val Asp Phe Glu Gly Pro Ala Val Ala Pro Thr Ser Gly Val Ala Gly
145 150 155 160

Leu Lys Ala Gly Leu Leu Val Thr Val Gly Val Leu Gly Leu Phe
165 170 175

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gagaactaca atcattgggc tcaaaggaat agattccaag tcaatgatac tctcttttc 180
aagtacaaga aagggtcaga ctcggtgctg ttggtaacaa gagaagatta cttctcatgc 240
aacaccaaga acccaattca gtcttaaca gaaggtgatt cactcttac atttgatcgg 300
tcgggtccct tcttttcat caccgtaac gctgataatt gcaaaaagg gcaaaagctg 360
atcgtcgtgg tcatggctgt aagacacaaa ccccagcaac aaccctccttc accttctccc 420
tcatctgctg tgacaacagc gccggttct ccacccacat taccattcc tgaaactaac 480
cctcctgttag agtcaccaaa gagcagttag gctccatctc atgatgctgt ggaaccagct 540
ccgccccggc acagatcggg ttcattcaaa ctagtatgtt ctacctggct ggtgtgggt 600
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20 25 30

Asp Gly Trp Val Val Ser Pro Ser Glu Asn Tyr Asn His Trp Ala Glu
35 40 45

Arg Asn Arg Phe Gln Val Asn Asp Thr Leu Phe Phe Lys Tyr Lys Lys
50 55 60

Gly Ser Asp Ser Val Leu Leu Val Thr Arg Glu Asp Tyr Phe Ser Cys
65 70 75 80

Asn Thr Lys Asn Pro Ile Gln Ser Leu Thr Glu Gly Asp Ser Leu Phe
85 90 95

Thr Phe Asp Arg Ser Gly Pro Phe Phe Phe Ile Thr Gly Asn Ala Asp
100 105 110

Asn Cys Lys Lys Gly Gln Lys Leu Ile Val Val Val Met Ala Val Arg
115 120 125

His Lys Pro Gln Gln Pro Pro Ser Pro Ser Pro Ser Ser Ala Val
130 135 140

Thr Thr Ala Pro Val Ser Pro Pro Thr Leu Pro Ile Pro Glu Thr Asn
145 150 155 160

Pro Pro Val Glu Ser Pro Lys Ser Ser Glu Ala Pro Ser His Asp Ala
165 170 175

Val Glu Pro Ala Pro Pro Glu His Arg Ser Gly Ser Phe Lys Leu Val
180 185 190

Cys Ser Thr Trp Leu Val Leu Gly Phe Gly Ile Trp Val Ser Met Ala
195 200 205

Leu Gly Ile Glu Asn Val Val Cys Phe Trp Cys
210 215

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<400> 22
ctagattcca atgtacctat gctttgaga c 31

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Tyr Lys Lys Ala Gly Ser Ala Ala Ala Pro Phe Thr Leu Val Pro Arg

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Gly Ser Lys Glu Ile Met Val Gly Gly Lys Thr Gly Ala Trp Lys Ile
35 40 45

Pro Ser Ser Glu Ser Asp Ser Leu Asn Lys Trp Ala Glu Lys Ala Arg
50 55 60

Phe Gln Ile Gly Asp Ser Leu Val Trp Lys Tyr Asp Gly Gly Lys Asp
65 70 75 80

Ser Val Leu Gln Val Ser Lys Glu Asp Tyr Thr Ser Cys Asn Thr Ser
85 90 95

Asn Pro Ile Ala Glu Tyr Lys Asp Gly Asn Thr Lys Val Lys Leu Glu
100 105 110

Lys Ser Gly Pro Tyr Phe Phe Met Ser Gly Ala Lys Gly His Cys Glu
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Gln Gly Arg Lys Met Ile Val Val Val Met Ser Gln Lys His Arg Tyr
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Ile Gly Ile
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20 25 30

Gly Ser Tyr Lys Phe Tyr Val Gly Gly Arg Asp Gly Trp Val Val Ser
35 40 45

Pro Ser Glu Asn Tyr Asn His Trp Ala Glu Arg Asn Arg Phe Gln Val
50 55 60

Asn Asp Thr Leu Phe Phe Lys Tyr Lys Lys Gly Ser Asp Ser Val Leu
65 70 75 80

123-03_US_second_replacement_sequence.txt

Leu Val Thr Arg Glu Asp Tyr Phe Ser Cys Asn Thr Lys Asn Pro Ile
85 90 95

Gln Ser Leu Thr Glu Gly Asp Ser Leu Phe Thr Phe Asp Arg Ser Gly
100 105 110

Pro Phe Phe Phe Ile Thr Gly Asn Ala Asp Asn Cys Lys Lys Gly Gln
115 120 125

Lys Leu Ile Val Val Val Met Ala Val Arg His Lys Pro Gln Gln Gln
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